

SEQUENCE LISTING

<110> Meyers, Rachel
Hunter, John Joseph

<120> 62112, A NOVEL HUMAN DEHYDROGENASE AND
USES THEREOF

<130> MNI-187

<150> 60/229,831

<151> 2000-08-31

<160> 3

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 2452

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (67)...(1932)

<400> 1

```

cgtgtgtgtg tccctgcggc gctaagaagg ggagactgag gctgaggctg gggaacatcg 60
ggcagc atg agc ggc tgc ggg ctc ttc ctg cgc acc acg gct gcg gct 108
      Met Ser Gly Cys Gly Leu Phe Leu Arg Thr Thr Ala Ala Ala
        1             5             10

cgt gcc tgc cgg ggt ctg gtg gtc tct acc gcg aac cgg cgg cta ctg 156
Arg Ala Cys Arg Gly Leu Val Val Ser Thr Ala Asn Arg Arg Leu Leu
  15             20             25             30

cgc acc agc ccg cct gta cga gct ttc gcc aaa gag ctt ttc cta ggc 204
Arg Thr Ser Pro Pro Val Arg Ala Phe Ala Lys Glu Leu Phe Leu Gly
          35             40             45

aaa atc aag aag aaa gaa gtt ttc cca ttt cca gaa gtt agc caa gat 252
Lys Ile Lys Lys Lys Glu Val Phe Pro Phe Pro Glu Val Ser Gln Asp
          50             55             60

gaa ctt aat gaa atc aat cag ttc ttg gga ccc gtg gaa aaa ttc ttc 300
Glu Leu Asn Glu Ile Asn Gln Phe Leu Gly Pro Val Glu Lys Phe Phe
        65             70             75

act gaa gag gtg gac tcc cga aaa att gac cag gaa ggg aaa atc cca 348
Thr Glu Glu Val Asp Ser Arg Lys Ile Asp Gln Glu Gly Lys Ile Pro
      80             85             90

gat gaa act ttg gag aaa ttg aag agc cta ggg ctt ttt ggg ctg caa 396
Asp Glu Thr Leu Glu Lys Leu Lys Ser Leu Gly Leu Phe Gly Leu Gln
     95             100             105             110

gtc cca gaa gaa tat ggt ggc ctg ggc ttc tcc aac acc atg tac tca 444
Val Pro Glu Glu Tyr Gly Gly Leu Gly Phe Ser Asn Thr Met Tyr Ser
          115             120             125

```

"FASTA" format

aga cta ggg gag atc atc agc atg gat ggg tcc atc act gtg acc ctg 492
 Arg Leu Gly Glu Ile Ile Ser Met Asp Gly Ser Ile Thr Val Thr Leu
 130 135 140

gca gcg cac cag gct att ggc ctc aag ggg atc atc ttg gct ggc act 540
 Ala Ala His Gln Ala Ile Gly Leu Lys Gly Ile Ile Leu Ala Gly Thr
 145 150 155

gag gag cag aaa gcc aaa tac ttg cct aaa ctg gcg tcc ggg gag cac 588
 Glu Glu Gln Lys Ala Lys Tyr Leu Pro Lys Leu Ala Ser Gly Glu His
 160 165 170

att gca gcc ttc tgc ctc acg gag cca gcc agt ggg agc gat gca gcc 636
 Ile Ala Ala Phe Cys Leu Thr Glu Pro Ala Ser Gly Ser Asp Ala Ala
 175 180 185 190

tca atc cgg agc aga gcc aca cta agt gaa gac aag aag cac tac atc 684
 Ser Ile Arg Ser Arg Ala Thr Leu Ser Glu Asp Lys Lys His Tyr Ile
 195 200 205

ctc aat ggc tcc aag gtc tgg att act aat gga gga ctg gcc aat att 732
 Leu Asn Gly Ser Lys Val Trp Ile Thr Asn Gly Gly Leu Ala Asn Ile
 210 215 220

ttt act gtg ttt gca aag act gag gtc gtt gat tct gat gga tca gtg 780
 Phe Thr Val Phe Ala Lys Thr Glu Val Val Asp Ser Asp Gly Ser Val
 225 230 235

aaa gac aaa atc aca gca ttc ata gta gaa aga gac ttt ggt gga gtc 828
 Lys Asp Lys Ile Thr Ala Phe Ile Val Glu Arg Asp Phe Gly Gly Val
 240 245 250

act aat ggg aaa ccc gaa gat aaa tta ggc att cgg ggc tcc aac act 876
 Thr Asn Gly Lys Pro Glu Asp Lys Leu Gly Ile Arg Gly Ser Asn Thr
 255 260 265 270

tgt gaa gtc cat ttt gaa aac acc aag ata cct gtg gaa aac atc ctt 924
 Cys Glu Val His Phe Glu Asn Thr Lys Ile Pro Val Glu Asn Ile Leu
 275 280 285

gga gag gtc gga gat ggg ttt aag gtg gcc atg aac atc ctc aac agc 972
 Gly Glu Val Gly Asp Gly Phe Lys Val Ala Met Asn Ile Leu Asn Ser
 290 295 300

ggc cgg ttc agc atg ggc agc gtc gtg gct ggg ctg ctc aag aga ttg 1020
 Gly Arg Phe Ser Met Gly Ser Val Val Ala Gly Leu Leu Lys Arg Leu
 305 310 315

att gaa atg act gct gag tac gcc tgc aca agg aaa cag ttt aac aag 1068
 Ile Glu Met Thr Ala Glu Tyr Ala Cys Thr Arg Lys Gln Phe Asn Lys
 320 325 330

agg ctc agt gaa ttt gga ttg att cag gag aaa ttt gca ctg atg gct 1116
 Arg Leu Ser Glu Phe Gly Leu Ile Gln Glu Lys Phe Ala Leu Met Ala
 335 340 345 350

cag aag gct tac gtc atg gag agt atg acc tac ctc aca gca ggg atg 1164
 Gln Lys Ala Tyr Val Met Glu Ser Met Thr Tyr Leu Thr Ala Gly Met
 355 360 365

ctg gac caa cct ggc ttt ccc gac tgc tcc atc gag gca gcc atg gtg 1212

09945326-033401

Leu	Asp	Gln	Pro	Gly	Phe	Pro	Asp	Cys	Ser	Ile	Glu	Ala	Ala	Met	Val		
			370					375						380			
aag	gtg	ttc	agc	tcc	gag	gcc	gcc	tgg	cag	tgt	gtg	agt	gag	gcg	ctg	1260	
Lys	Val	Phe	Ser	Ser	Glu	Ala	Ala	Trp	Gln	Cys	Val	Ser	Glu	Ala	Leu		
		385					390					395					
cag	atc	ctc	ggg	ggc	ttg	ggc	tac	aca	agg	gac	tat	ccg	tac	gag	cgc	1308	
Gln	Ile	Leu	Gly	Gly	Leu	Gly	Tyr	Thr	Arg	Asp	Tyr	Pro	Tyr	Glu	Arg		
	400					405					410						
ata	ctg	cgt	gac	acc	cgc	atc	ctc	ctc	atc	ttc	gag	gga	acc	aat	gag	1356	
Ile	Leu	Arg	Asp	Thr	Arg	Ile	Leu	Leu	Ile	Phe	Glu	Gly	Thr	Asn	Glu		
	415				420				425						430		
att	ctc	cgg	atg	tac	atc	gcc	ctg	acg	ggg	ctg	cag	cat	gcc	ggc	cgc	1404	
Ile	Leu	Arg	Met	Tyr	Ile	Ala	Leu	Thr	Gly	Leu	Gln	His	Ala	Gly	Arg		
			435					440						445			
atc	ctg	act	acc	agg	atc	cat	gag	ctt	aaa	cag	gcc	aaa	gtg	agc	aca	1452	
Ile	Leu	Thr	Thr	Arg	Ile	His	Glu	Leu	Lys	Gln	Ala	Lys	Val	Ser	Thr		
			450				455						460				
gtc	atg	gat	acc	gtt	ggc	cgg	agg	ctt	cgg	gac	tcc	ctg	ggc	cga	act	1500	
Val	Met	Asp	Thr	Val	Gly	Arg	Arg	Leu	Arg	Asp	Ser	Leu	Gly	Arg	Thr		
		465				470						475					
gtg	gac	ctg	ggg	ctg	aca	ggc	aac	cat	gga	gtt	gtg	cac	ccc	agt	ctt	1548	
Val	Asp	Leu	Gly	Leu	Thr	Gly	Asn	His	Gly	Val	Val	His	Pro	Ser	Leu		
	480					485				490							
gcg	gac	agt	gcc	aac	aag	ttt	gag	gag	aac	acc	tac	tgc	ttc	ggc	cgc	1596	
Ala	Asp	Ser	Ala	Asn	Lys	Phe	Glu	Glu	Asn	Thr	Tyr	Cys	Phe	Gly	Arg		
	495			500					505						510		
acc	gtg	gag	aca	ctg	ctg	ctc	cgc	ttt	ggc	aag	acc	atc	atg	gag	gag	1644	
Thr	Val	Glu	Thr	Leu	Leu	Leu	Arg	Phe	Gly	Lys	Thr	Ile	Met	Glu	Glu		
			515				520							525			
cag	ctg	gta	ctg	aag	cgg	gtg	gcc	aac	atc	ctc	atc	aac	ctg	tat	ggc	1692	
Gln	Leu	Val	Leu	Lys	Arg	Val	Ala	Asn	Ile	Leu	Ile	Asn	Leu	Tyr	Gly		
		530					535						540				
atg	acg	gcc	gtg	ctg	tcg	cgg	gcc	agc	cgc	tcc	atc	cgc	att	ggg	ctc	1740	
Met	Thr	Ala	Val	Leu	Ser	Arg	Ala	Ser	Arg	Ser	Ile	Arg	Ile	Gly	Leu		
		545				550						555					
cgc	aac	cac	gac	cac	gag	gtt	ctc	ttg	gcc	aac	acc	ttc	tgc	gtg	gaa	1788	
Arg	Asn	His	Asp	His	Glu	Val	Leu	Leu	Ala	Asn	Thr	Phe	Cys	Val	Glu		
	560					565				570							
gct	tac	ttg	cag	aat	ctc	ttc	agc	ctc	tct	cag	ctg	gac	aag	tat	gct	1836	
Ala	Tyr	Leu	Gln	Asn	Leu	Phe	Ser	Leu	Ser	Gln	Leu	Asp	Lys	Tyr	Ala		
	575				580				585						590		
cca	gaa	aac	cta	gat	gag	cag	att	aag	aaa	gtg	tcc	cag	cag	atc	ctt	1884	
Pro	Glu	Asn	Leu	Asp	Glu	Gln	Ile	Lys	Lys	Val	Ser	Gln	Gln	Ile	Leu		
			595					600						605			
gag	aag	cga	gcc	tat	atc	tgt	gcc	cac	cct	ctg	gac	agg	aca	tgc	tga	1932	
Glu	Lys	Arg	Ala	Tyr	Ile	Cys	Ala	His	Pro	Leu	Asp	Arg	Thr	Cys	*		

094536-033401

610

615

620

```

ggcagggggac agtgtccctt gctaccgccc gcccctaccc atggcccgtt gctggatgac 1992
tggtactctt ttttcagaag gtgttgggat taccacaggt taagcctttt gttccccgtc 2052
tgcacctgaa ggggtgtcgc ctggcctggg agagcctctt ccagggtttg acctgcaggc 2112
agtgtctctt aacaggacca tcacagcttc tgaactgagc cggagagaga gaatggaatt 2172
gctgacctct ggaactggcg ggtattctgg tcattgagga gacaccatag tggaaactgg 2232
ggcttatgct gctgcctcca ggggtgtgagg tgggtgggga cctgtgtcag gtgtggatag 2292
ccatttctgc tcaaccacac attctctaag aaacagcttg aaagctctgt ctgggtcatt 2352
catttaaaact agaagcagag gcacttaaaa catgtaccag gaaccattta acaaagaata 2412
taaaatgtca caatctgtgt actgttaaaa aaaaaaaaaa 2452

```

<210> 2

<211> 621

<212> PRT

<213> Homo sapiens

<400> 2

```

Met Ser Gly Cys Gly Leu Phe Leu Arg Thr Thr Ala Ala Ala Arg Ala
 1          5          10          15
Cys Arg Gly Leu Val Val Ser Thr Ala Asn Arg Arg Leu Leu Arg Thr
 20          25          30
Ser Pro Pro Val Arg Ala Phe Ala Lys Glu Leu Phe Leu Gly Lys Ile
 35          40          45
Lys Lys Lys Glu Val Phe Pro Phe Pro Glu Val Ser Gln Asp Glu Leu
 50          55          60
Asn Glu Ile Asn Gln Phe Leu Gly Pro Val Glu Lys Phe Phe Thr Glu
 65          70          75          80
Glu Val Asp Ser Arg Lys Ile Asp Gln Glu Gly Lys Ile Pro Asp Glu
 85          90          95
Thr Leu Glu Lys Leu Lys Ser Leu Gly Leu Phe Gly Leu Gln Val Pro
100          105          110
Glu Glu Tyr Gly Gly Leu Gly Phe Ser Asn Thr Met Tyr Ser Arg Leu
115          120          125
Gly Glu Ile Ile Ser Met Asp Gly Ser Ile Thr Val Thr Leu Ala Ala
130          135          140
His Gln Ala Ile Gly Leu Lys Gly Ile Ile Leu Ala Gly Thr Glu Glu
145          150          155          160
Gln Lys Ala Lys Tyr Leu Pro Lys Leu Ala Ser Gly Glu His Ile Ala
165          170          175
Ala Phe Cys Leu Thr Glu Pro Ala Ser Gly Ser Asp Ala Ala Ser Ile
180          185          190
Arg Ser Arg Ala Thr Leu Ser Glu Asp Lys Lys His Tyr Ile Leu Asn
195          200          205
Gly Ser Lys Val Trp Ile Thr Asn Gly Gly Leu Ala Asn Ile Phe Thr
210          215          220
Val Phe Ala Lys Thr Glu Val Val Asp Ser Asp Gly Ser Val Lys Asp
225          230          235          240
Lys Ile Thr Ala Phe Ile Val Glu Arg Asp Phe Gly Gly Val Thr Asn
245          250          255
Gly Lys Pro Glu Asp Lys Leu Gly Ile Arg Gly Ser Asn Thr Cys Glu
260          265          270
Val His Phe Glu Asn Thr Lys Ile Pro Val Glu Asn Ile Leu Gly Glu
275          280          285
Val Gly Asp Gly Phe Lys Val Ala Met Asn Ile Leu Asn Ser Gly Arg
290          295          300
Phe Ser Met Gly Ser Val Val Ala Gly Leu Leu Lys Arg Leu Ile Glu
305          310          315          320
Met Thr Ala Glu Tyr Ala Cys Thr Arg Lys Gln Phe Asn Lys Arg Leu
325          330          335
Ser Glu Phe Gly Leu Ile Gln Glu Lys Phe Ala Leu Met Ala Gln Lys

```

			340					345					350			
Ala	Tyr	Val	Met	Glu	Ser	Met	Thr	Tyr	Leu	Thr	Ala	Gly	Met	Leu	Asp	
		355					360					365				
Gln	Pro	Gly	Phe	Pro	Asp	Cys	Ser	Ile	Glu	Ala	Ala	Met	Val	Lys	Val	
		370				375					380					
Phe	Ser	Ser	Glu	Ala	Ala	Trp	Gln	Cys	Val	Ser	Glu	Ala	Leu	Gln	Ile	
385					390					395					400	
Leu	Gly	Gly	Leu	Gly	Tyr	Thr	Arg	Asp	Tyr	Pro	Tyr	Glu	Arg	Ile	Leu	
				405					410					415		
Arg	Asp	Thr	Arg	Ile	Leu	Leu	Ile	Phe	Glu	Gly	Thr	Asn	Glu	Ile	Leu	
			420					425					430			
Arg	Met	Tyr	Ile	Ala	Leu	Thr	Gly	Leu	Gln	His	Ala	Gly	Arg	Ile	Leu	
			435				440					445				
Thr	Thr	Arg	Ile	His	Glu	Leu	Lys	Gln	Ala	Lys	Val	Ser	Thr	Val	Met	
					455						460					
Asp	Thr	Val	Gly	Arg	Arg	Leu	Arg	Asp	Ser	Leu	Gly	Arg	Thr	Val	Asp	
465					470					475					480	
Leu	Gly	Leu	Thr	Gly	Asn	His	Gly	Val	Val	His	Pro	Ser	Leu	Ala	Asp	
				485					490					495		
Ser	Ala	Asn	Lys	Phe	Glu	Glu	Asn	Thr	Tyr	Cys	Phe	Gly	Arg	Thr	Val	
			500					505					510			
Glu	Thr	Leu	Leu	Leu	Arg	Phe	Gly	Lys	Thr	Ile	Met	Glu	Glu	Gln	Leu	
			515				520					525				
Val	Leu	Lys	Arg	Val	Ala	Asn	Ile	Leu	Ile	Asn	Leu	Tyr	Gly	Met	Thr	
					535						540					
Ala	Val	Leu	Ser	Arg	Ala	Ser	Arg	Ser	Ile	Arg	Ile	Gly	Leu	Arg	Asn	
545					550					555					560	
His	Asp	His	Glu	Val	Leu	Leu	Ala	Asn	Thr	Phe	Cys	Val	Glu	Ala	Tyr	
				565					570					575		
Leu	Gln	Asn	Leu	Phe	Ser	Leu	Ser	Gln	Leu	Asp	Lys	Tyr	Ala	Pro	Glu	
			580					585					590			
Asn	Leu	Asp	Glu	Gln	Ile	Lys	Lys	Val	Ser	Gln	Gln	Ile	Leu	Glu	Lys	
		595					600					605				
Arg	Ala	Tyr	Ile	Cys	Ala	His	Pro	Leu	Asp	Arg	Thr	Cys				
		610				615					620					

```
<210> 3
<211> 1863
<212> DNA
<213> Homo sapiens
```

```
<220>
<221> CDS
<222> (1)...(1863)
```

<400> 3																	
atg	agc	ggc	tgc	ggg	ctc	ttc	ctg	cgc	acc	acg	gct	gcg	gct	cgt	gcc	48	
Met	Ser	Gly	Cys	Gly	Leu	Phe	Leu	Arg	Thr	Thr	Ala	Ala	Ala	Arg	Ala		
1		5			10					15							
.																	
tgc	cgg	ggt	ctg	gtg	gtc	tct	acc	gcg	aac	cgg	cgg	cta	ctg	cgc	acc	96	
Cys	Arg	Gly	Leu	Val	Val	Ser	Thr	Ala	Asn	Arg	Arg	Leu	Leu	Arg	Thr		
			20		25					30							
.																	
agc	ccg	cct	gta	cga	gct	ttc	gcc	aaa	gag	ctt	ttc	cta	ggc	aaa	atc	144	
Ser	Pro	Pro	Val	Arg	Ala	Phe	Ala	Lys	Glu	Leu	Phe	Leu	Gly	Lys	Ile		
		35			40					45							
.																	
aag	aag	aaa	gaa	gtt	ttc	cca	ttt	cca	gaa	gtt	agc	caa	gat	gaa	ctt	192	
Lys	Lys	Lys	Glu	Val	Phe	Pro	Phe	Pro	Glu	Val	Ser	Gln	Asp	Glu	Leu		

50	55	60	
aat gaa atc aat cag ttc ttg gga ccc gtg gaa aaa ttc ttc act gaa			240
Asn Glu Ile Asn Gln Phe Leu Gly Pro Val Glu Lys Phe Phe Thr Glu			
65	70	75	80
gag gtg gac tcc cga aaa att gac cag gaa ggg aaa atc cca gat gaa			288
Glu Val Asp Ser Arg Lys Ile Asp Gln Glu Gly Lys Ile Pro Asp Glu			
	85	90	95
act ttg gag aaa ttg aag agc cta ggg ctt ttt ggg ctg caa gtc cca			336
Thr Leu Glu Lys Leu Lys Ser Leu Gly Leu Phe Gly Leu Gln Val Pro			
	100	105	110
gaa gaa tat ggt ggc ctg ggc ttc tcc aac acc atg tac tca aga cta			384
Glu Glu Tyr Gly Gly Leu Gly Phe Ser Asn Thr Met Tyr Ser Arg Leu			
	115	120	125
ggg gag atc atc agc atg gat ggg tcc atc act gtg acc ctg gca gcg			432
Gly Glu Ile Ile Ser Met Asp Gly Ser Ile Thr Val Thr Leu Ala Ala			
	130	135	140
cac cag gct att ggc ctc aag ggg atc atc ttg gct ggc act gag gag			480
His Gln Ala Ile Gly Leu Lys Gly Ile Ile Leu Ala Gly Thr Glu Glu			
	145	150	155
cag aaa gcc aaa tac ttg cct aaa ctg gcg tcc ggg gag cac att gca			528
Gln Lys Ala Lys Tyr Leu Pro Lys Leu Ala Ser Gly Glu His Ile Ala			
	165	170	175
gcc ttc tgc ctc acg gag cca gcc agt ggg agc gat gca gcc tca atc			576
Ala Phe Cys Leu Thr Glu Pro Ala Ser Gly Ser Asp Ala Ala Ser Ile			
	180	185	190
cgg agc aga gcc aca cta agt gaa gac aag aag cac tac atc ctc aat			624
Arg Ser Arg Ala Thr Leu Ser Glu Asp Lys Lys His Tyr Ile Leu Asn			
	195	200	205
ggc tcc aag gtc tgg att act aat gga gga ctg gcc aat att ttt act			672
Gly Ser Lys Val Trp Ile Thr Asn Gly Gly Leu Ala Asn Ile Phe Thr			
	210	215	220
gtg ttt gca aag act gag gtc gtt gat tct gat gga tca gtg aaa gac			720
Val Phe Ala Lys Thr Glu Val Val Asp Ser Asp Gly Ser Val Lys Asp			
	225	230	235
aaa atc aca gca ttc ata gta gaa aga gac ttt ggt gga gtc act aat			768
Lys Ile Thr Ala Phe Ile Val Glu Arg Asp Phe Gly Gly Val Thr Asn			
	245	250	255
ggg aaa ccc gaa gat aaa tta ggc att cgg ggc tcc aac act tgt gaa			816
Gly Lys Pro Glu Asp Lys Leu Gly Ile Arg Gly Ser Asn Thr Cys Glu			
	260	265	270
gtc cat ttt gaa aac acc aag ata cct gtg gaa aac atc ctt gga gag			864
Val His Phe Glu Asn Thr Lys Ile Pro Val Glu Asn Ile Leu Gly Glu			
	275	280	285
gtc gga gat ggg ttt aag gtg gcc atg aac atc ctc aac agc ggc cgg			912
Val Gly Asp Gly Phe Lys Val Ala Met Asn Ile Leu Asn Ser Gly Arg			
	290	295	300

09945326-083101

ttc agc atg ggc agc gtc gtg gct ggg ctg ctc aag aga ttg att gaa 960
 Phe Ser Met Gly Ser Val Val Ala Gly Leu Leu Lys Arg Leu Ile Glu
 305 310 315 320

atg act gct gag tac gcc tgc aca agg aaa cag ttt aac aag agg ctc 1008
 Met Thr Ala Glu Tyr Ala Cys Thr Arg Lys Gln Phe Asn Lys Arg Leu
 325 330 335

agt gaa ttt gga ttg att cag gag aaa ttt gca ctg atg gct cag aag 1056
 Ser Glu Phe Gly Leu Ile Gln Glu Lys Phe Ala Leu Met Ala Gln Lys
 340 345 350

gct tac gtc atg gag agt atg acc tac ctc aca gca ggg atg ctg gac 1104
 Ala Tyr Val Met Glu Ser Met Thr Tyr Leu Thr Ala Gly Met Leu Asp
 355 360 365

caa cct ggc ttt ccc gac tgc tcc atc gag gca gcc atg gtg aag gtg 1152
 Gln Pro Gly Phe Pro Asp Cys Ser Ile Glu Ala Ala Met Val Lys Val
 370 375 380

ttc agc tcc gag gcc gcc tgg cag tgt gtg agt gag gcg ctg cag atc 1200
 Phe Ser Ser Glu Ala Ala Trp Gln Cys Val Ser Glu Ala Leu Gln Ile
 385 390 395 400

ctc ggg ggc ttg ggc tac aca agg gac tat ccg tac gag cgc ata ctg 1248
 Leu Gly Gly Leu Gly Tyr Thr Arg Asp Tyr Pro Tyr Glu Arg Ile Leu
 405 410 415

cgt gac acc cgc atc ctc ctc atc ttc gag gga acc aat gag att ctc 1296
 Arg Asp Thr Arg Ile Leu Leu Ile Phe Glu Gly Thr Asn Glu Ile Leu
 420 425 430

cgg atg tac atc gcc ctg acg ggt ctg cag cat gcc ggc cgc atc ctg 1344
 Arg Met Tyr Ile Ala Leu Thr Gly Leu Gln His Ala Gly Arg Ile Leu
 435 440 445

act acc agg atc cat gag ctt aaa cag gcc aaa gtg agc aca gtc atg 1392
 Thr Thr Arg Ile His Glu Leu Lys Gln Ala Lys Val Ser Thr Val Met
 450 455 460

gat acc gtt ggc cgg agg ctt cgg gac tcc ctg ggc cga act gtg gac 1440
 Asp Thr Val Gly Arg Arg Leu Arg Asp Ser Leu Gly Arg Thr Val Asp
 465 470 475 480

ctg ggg ctg aca ggc aac cat gga gtt gtg cac ccc agt ctt gcg gac 1488
 Leu Gly Leu Thr Gly Asn His Gly Val Val His Pro Ser Leu Ala Asp
 485 490 495

agt gcc aac aag ttt gag gag aac acc tac tgc ttc ggc cgg acc gtg 1536
 Ser Ala Asn Lys Phe Glu Glu Asn Thr Tyr Cys Phe Gly Arg Thr Val
 500 505 510

gag aca ctg ctg ctc cgc ttt ggc aag acc atc atg gag gag cag ctg 1584
 Glu Thr Leu Leu Leu Arg Phe Gly Lys Thr Ile Met Glu Glu Gln Leu
 515 520 525

gta ctg aag cgg gtg gcc aac atc ctc atc aac ctg tat ggc atg acg 1632
 Val Leu Lys Arg Val Ala Asn Ile Leu Ile Asn Leu Tyr Gly Met Thr
 530 535 540

000445330 003404
 000445330 003404

gcc	gtg	ctg	tcg	cgg	gcc	agc	cgc	tcc	atc	cgc	att	ggg	ctc	cgc	aac	1680
Ala	Val	Leu	Ser	Arg	Ala	Ser	Arg	Ser	Ile	Arg	Ile	Gly	Leu	Arg	Asn	
545					550					555					560	
cac	gac	cac	gag	gtt	ctc	ttg	gcc	aac	acc	ttc	tgc	gtg	gaa	gct	tac	1728
His	Asp	His	Glu	Val	Leu	Leu	Ala	Asn	Thr	Phe	Cys	Val	Glu	Ala	Tyr	
				565					570						575	
ttg	cag	aat	ctc	ttc	agc	ctc	tct	cag	ctg	gac	aag	tat	gct	cca	gaa	1776
Leu	Gln	Asn	Leu	Phe	Ser	Leu	Ser	Gln	Leu	Asp	Lys	Tyr	Ala	Pro	Glu	
			580					585					590			
aac	cta	gat	gag	cag	att	aag	aaa	gtg	tcc	cag	cag	atc	ctt	gag	aag	1824
Asn	Leu	Asp	Glu	Gln	Ile	Lys	Lys	Val	Ser	Gln	Gln	Ile	Leu	Glu	Lys	
		595					600					605				
cga	gcc	tat	atc	tgt	gcc	cac	cct	ctg	gac	agg	aca	tgc				1863
Arg	Ala	Tyr	Ile	Cys	Ala	His	Pro	Leu	Asp	Arg	Thr	Cys				
	610					615						620				

00945326 003101